

~~07040590~~

~~04/001PE #9~~

CRF Errors Corrected by the STIC Systems Branch

Sortal Number: 09/677,374

CRF Processing Date:

Edited by:

Verified by:

10/23/2001

Changed a file from non-ASCII to ASCII

ENTERED

Changed the margins in cases where the sequence text was 'wrapped' down to the next line.

Edited a formal error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for 'Current Application Data'.

Edited the 'Number of Sequences' field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

12

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: ..

Deleted extra, invalid, headings used by an applicant, specifically:

(Inventor)

Deleted: non-ASCII 'garbage' at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A 'Hard Page Break' code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the '(A)Length:' field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other:

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/677,374

DATE: 10/23/2001
 TIME: 13:42:45

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF3\10232001\I677374.raw

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3 <110> APPLICANT: Burian, Jan
4     Kuzyk, Michael
5     Thornton, Julian
6     Kay, William
8 <120> TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
9     RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
11 <130> FILE REFERENCE: IDC01/60485/US
13 <140> CURRENT APPLICATION NUMBER: US 09/677,374
14 <141> CURRENT FILING DATE: 2000-09-15
16 <150> PRIOR APPLICATION NUMBER: US 60/154,437
17 <151> PRIOR FILING DATE: 1999-09-17
19 <150> PRIOR APPLICATION NUMBER: NO 20004637
20 <151> PRIOR FILING DATE: 2000-09-15
22 <150> PRIOR APPLICATION NUMBER: IE 2000/0752
23 <151> PRIOR FILING DATE: 2000-09-18
25 <150> PRIOR APPLICATION NUMBER: GB 0022825.4
26 <151> PRIOR FILING DATE: 2000-09-18
28 <150> PRIOR APPLICATION NUMBER: CL 2544-2000
29 <151> PRIOR FILING DATE: 2000-09-15
31 <160> NUMBER OF SEQ ID NOS: 20
33 <170> SOFTWARE: PatentIn version 3.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 486
37 <212> TYPE: DNA
38 <213> ORGANISM: Piscirickettsia salmonis
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(486)
45 <400> SEQUENCE: 1
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47 Met Asn Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val
48 1           5           10          15
50 ttt tta gtt ggc tgt gcc cag aac ttt agt cgt caa gaa gtc gga gct 96
51 Phe Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala
52           20          25          30
54 gcg act ggg gct gtt ggc ggt gtt gct ggc cag ctg ttt ggt aaa 144
55 Ala Thr Gly Ala Val Val Gly Val Ala Gly Gln Leu Phe Gly Lys
56           35          40          45
58 ggt agt ggt cga gtt gca atg gcc att ggt ggt gct gtt ttg ggt gga 192
59 Gly Ser Gly Arg Val Ala Met Ala Ile Gly Gly Ala Val Leu Gly Gly
60           50          55          60
62 tta att ggt tct aaa atc ggt caa tcg atg gat cag cag gat aaa ata 240
63 Leu Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile
64 65           70          75          80
66 aag cta aac cag agt ttg gaa aag gta aaa gca ggg caa gtg aca cgt 288
67 Lys Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg
68           85          90          95

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Input Set : A:\PTO.AMC.txt
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70 tgg cgt aat cca gat aca ggc aat agt tat agt gtt gag cca gtg cgt 336
 71 Trp Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg
 72 100 105 110
 74 act tac cag cgt tac aat aag caa gag cgt cgc cag caa tat tgt cga 384
 75 Thr Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg
 76 115 120 125
 78 gaa ttt cag caa aag gcg atg att gca ggg cag aag caa gag att tac 432
 79 Glu Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr
 80 130 135 140
 82 ggc act gca tgc cgg caa ccg gat ggt cgt tgg caa gtc att tca aca 480
 83 Gly Thr Ala Cys Arg Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr
 84 145 150 155 160
 86 gaa aaa 486
 87 Glu Lys
 90 <210> SEQ ID NO: 2
 91 <211> LENGTH: 162
 92 <212> TYPE: PRT
 93 <213> ORGANISM: Piscirickettsia salmonis
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 98 Met Asn Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val
 99 1 5 10 15
 101 Phe Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala
 102 20 25 30
 104 Ala Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys
 105 35 40 45
 107 Gly Ser Gly Arg Val Ala Met Ala Ile Gly Gly Ala Val Leu Gly Gly
 108 50 55 60
 110 Leu Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile
 111 65 70 75 80
 113 Lys Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg
 114 85 90 95
 116 Trp Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg
 117 100 105 110
 119 Thr Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg
 120 115 120 125
 122 Glu Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr
 123 130 135 140
 125 Gly Thr Ala Cys Arg Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr
 126 145 150 155 160
 128 Glu Lys
 131 <210> SEQ ID NO: 3
 132 <211> LENGTH: 483
 133 <212> TYPE: DNA
 134 <213> ORGANISM: Piscirickettsia salmonis
 136 <220> FEATURE:
 137 <221> NAME/KEY: CDS
 138 <222> LOCATION: (1)..(483)
 141 <400> SEQUENCE: 3
 142 atg cgt ggt tgc ctg cag ggc agc tct ctg atc att atc tct gtt ttc 48

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143 Met Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe
144 1 5 10 15
146 ctg gtg ggt tgc gcc cag aac ttc agc cgc cag gaa gtt ggc gcg gcc 96
147 Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala
148 20 25 30
150 acc ggt gcg gtt gtg ggc ggt gtt gcc ggc cag ctg ttc ggt aaa ggc 144
151 Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly
152 35 40 45
154 tct ggt cgt gtg tcg atg gcc atc ggc ggt gcg gtt ctg ggc ggt ctg 192
155 Ser Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu
156 50 55 60
158 att ggc tct aaa atc ggt cag agc atg gac cag cag gat aaa atc aaa 240
159 Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys
160 65 70 75 80
162 ctg aac cag tct ctg gaa aaa gtt gac ggc cag gtt act cgt tgg 288
163 Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp
164 85 90 95
166 cgt aat ccg gac acc ggt aac agc tac tct gtt gaa ccg gtt cgc acc 336
167 Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr
168 100 105 110
170 tac cag cgt tac aac aaa cag gaa cgc cgt cag cag tac tgc cgc gaa 384
171 Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu
172 115 120 125
174 ttt cag cag aaa gcc atg atc gca ggt cag aaa cag gaa atc tac ggc 432
175 Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly
176 130 135 140
178 acc gcg tgc cct cag ccg gat ggc cgc tgg cag gtt att agc acc gaa 480
179 Thr Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu
180 145 150 155 160
182 aaa 483
183 Lys
186 <210> SEQ ID NO: 4
187 <211> LENGTH: 161
188 <212> TYPE: PRT
189 <213> ORGANISM: Piscirickettsia salmonis
192 <400> SEQUENCE: 4
194 Met Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ile Ser Val Phe
195 1 5 10 15
197 Leu Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala
198 20 25 30
200 Thr Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly
201 35 40 45
203 Ser Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu
204 50 55 60
206 Ile Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys
207 65 70 75 80
209 Leu Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp
210 85 90 95
212 Arg Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr

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213          100          105          110
215 Tyr Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu
216          115          120          125
218 Phe Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly
219          130          135          140
221 Thr Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu
222 145          150          155          160
224 Lys
227 <210> SEQ ID NO: 5
228 <211> LENGTH: 768
229 <212> TYPE: DNA
230 <213> ORGANISM: Piscirickettsia salmonis
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (1)..(768)
236 <220> FEATURE:
237 <221> NAME/KEY: sig_peptide
238 <222> LOCATION: (1)..(285)
240 <220> FEATURE:
241 <221> NAME/KEY: mat_peptide
242 <222> LOCATION: (286)..(768)
245 <400> SEQUENCE: 5
246 atg tca gtt gaa ttc tac aac tct aac aaa tca gca caa aca aac tca 48
247 Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
248 -95          -90          -85          -80
250 att aca cca ata atc aaa att act aac aca tct gac agt gat tta aat 96
251 Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
252          -75          -70          -65
254 tta aat gac gta aaa gtt aga tat tat tac aca agt gat ggt aca caa 144
255 Leu Asn Asp Val Lys Val Arg Tyr Tyr Thr Ser Asp Gly Thr Gln
256          -60          -55          -50
258 gga caa act ttc tgg tgt gac cat gct ggt gca tta tta gga aat agc 192
259 Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
260          -45          -40          -35
262 tat gtt gat aac act agc aaa gtg aca gca aac ttc gtt aaa gaa aca 240
263 Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
264          -30          -25          -20
266 gca agc cca aca tca acc tat gat aca tat ctg gat ccg tct cat atg 288
267 Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Leu Asp Pro Ser His Met
268 -15          -10          -5          1
270 cgt ggt tgc ctg cag ggc agc tct ctg atc att atc tct gtt ttc ctg 336
271 Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ser Val Phe Leu
272          5           10          15
274 gtg ggt tgc gcc cag aac ttc agc cgc cag gaa gtt ggc gcg gcc acc 384
275 Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala Thr
276          20          25          30
278 ggt gcg gtt gtg ggc ggt gtt gcc ggc cag ctg ttc ggt aaa ggc tct 432
279 Gly Ala Val Val Gly Gly Val Ala Gly Gln Leu Phe Gly Lys Gly Ser
280          35          40          45

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282 ggt cgt gtg tcg atg gcc atc ggc ggt gcg gtt ctg ggc ggt ctg att 480
283 Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu Ile
284 50           55           60           65
286 ggc tct aaa atc ggt cag agc atg gac cag cag gat aaa atc aaa ctg 528
287 Gly Ser Lys Ile Gly Gln Ser Met Asp Gln Gln Asp Lys Ile Lys Leu
288           70           75           80
290 aac cag tct ctg gaa aaa gtc gaa gcc ggc cag gtt act cgt tgg cgt 576
291 Asn Gln Ser Leu Glu Lys Val Lys Ala Gly Gln Val Thr Arg Trp Arg
292           85           90           95
294 aat ccg gac acc ggt aac agc tac tct gtc gaa ccg gtt cgc acc tac 624
295 Asn Pro Asp Thr Gly Asn Ser Tyr Ser Val Glu Pro Val Arg Thr Tyr
296           100          105          110
298 cag cgt tac aac aaa cag gaa ccg cgt cag cag tac tgc cgc gaa ttt 672
299 Gln Arg Tyr Asn Lys Gln Glu Arg Arg Gln Gln Tyr Cys Arg Glu Phe
300           115          120          125
302 cag cag aaa gcc atg atc gca ggt cag aaa cag gaa atc tac ggc acc 720
303 Gln Gln Lys Ala Met Ile Ala Gly Gln Lys Gln Glu Ile Tyr Gly Thr
304           130          135          140          145
306 gcg tgc cct cag ccg gat ggc cgc tgg cag gtc att agc acc gaa aaa 768
307 Ala Cys Pro Gln Pro Asp Gly Arg Trp Gln Val Ile Ser Thr Glu Lys
308           150          155          160
311 <210> SEQ ID NO: 6
312 <211> LENGTH: 256
313 <212> TYPE: PRT
314 <213> ORGANISM: Piscirickettsia salmonis
316 <220> FEATURE:
317 <221> NAME/KEY: SIGNAL
318 <222> LOCATION: (-95)..(-1)
321 <400> SEQUENCE: 6
323 Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
324 -95           -90           -85           -80
326 Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
327           -75           -70           -65
329 Leu Asn Asp Val Lys Val Arg Tyr Tyr Thr Ser Asp Gly Thr Gln
330           -60           -55           -50
332 Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
333           -45           -40           -35
335 Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
336           -30           -25           -20
338 Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Leu Asp Pro Ser His Met
339 -15           -10           -5            1
341 Arg Gly Cys Leu Gln Gly Ser Ser Leu Ile Ile Ser Val Phe Leu
342           5            10           15
344 Val Gly Cys Ala Gln Asn Phe Ser Arg Gln Glu Val Gly Ala Ala Thr
345           20           25           30
347 Gly Ala Val Val Gly Val Ala Gly Gln Leu Phe Gly Lys Gly Ser
348           35           40           45
350 Gly Arg Val Ser Met Ala Ile Gly Gly Ala Val Leu Gly Gly Leu Ile
351           50           55           60           65

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VERIFICATION SUMMARY

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DATE: 10/23/2001

TIME: 13:42:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10232001\I677374.raw